

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

10/ 500, 671  
PCT  
1-26-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/500,671

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      **Wrapped Nucleics**  
**Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      **Misaligned Amino**  
**Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      **Variable Length** Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      **PatentIn 2.0**  
**"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      **Skipped Sequences**  
**(OLD RULES)** Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8      **Skipped Sequences**  
**(NEW RULES)** Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 9      **Use of n's or Xaa's**  
**(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      **Invalid <213>**  
**Response** Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.
- 11      **Use of <220>** Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      **PatentIn 2.0**  
**"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

## RAW SEQUENCE LISTING

DATE: 01/26/2005

PATENT APPLICATION: US/10/500,671

TIME: 12:29:27

Input Set : D:\1392-10-18-2.ST25.txt

Output Set: N:\CRF4\01262005\J500671.raw

3 <110> APPLICANT: Sera, Takashi  
 5 <120> TITLE OF INVENTION: Nuclear-Envelope and Nuclear-Lamina Binding Chimeras for  
 6 Modulating Gene Expression  
 8 <130> FILE REFERENCE: 109845-163  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/500,671  
 C--> 10 <141> CURRENT FILING DATE: 2004-07-02  
 10 <160> NUMBER OF SEQ ID NOS: 18  
 12 <170> SOFTWARE: PatentIn version 3.2  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 25  
 16 <212> TYPE: PRT  
 17 <213> ORGANISM: Artificial  
 19 <220> FEATURE:  
 20 <223> OTHER INFORMATION: Zinc finger domain  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: MISC\_FEATURE  
 25 <222> LOCATION: (2)..(5)  
 26 <223> OTHER INFORMATION: Amino acids 2-5 are Xaa wherein Xaa = any amino acid, and up  
 to  
 27 two amino acids can be missing.  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: MISC\_FEATURE  
 31 <222> LOCATION: (7)..(18)  
 32 <223> OTHER INFORMATION: Xaa can be any amino acid  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: MISC\_FEATURE  
 36 <222> LOCATION: (20)..(24)  
 37 <223> OTHER INFORMATION: Amino acids 20-24 are Xaa wherein Xaa = any amino acid, and  
 up to  
 38 two amino acids can be missing.  
 40 <400> SEQUENCE: 1  
 W--> 42 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 43 1 5 10 15  
 46 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His  
 47 20 25  
 50 <210> SEQ ID NO: 2  
 51 <211> LENGTH: 32  
 52 <212> TYPE: PRT  
 53 <213> ORGANISM: Artificial  
 55 <220> FEATURE:  
 56 <223> OTHER INFORMATION: Second zinc finger domain  
 59 <220> FEATURE:  
 60 <221> NAME/KEY: MISC\_FEATURE  
 61 <222> LOCATION: (1)..(3)

Does Not Comply  
 Corrected Diskette Needed  
 (pg. 5, 7)

62 <223> OTHER INFORMATION: Xaa can be any amino acid

## RAW SEQUENCE LISTING

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Input Set : D:\1392-10-18-2.ST25.txt

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64 <220> FEATURE:  
65 <221> NAME/KEY: MISC\_FEATURE  
66 <222> LOCATION: (5)..(8)  
67 <223> OTHER INFORMATION: Amino acids 5-8 are Xaa wherein Xaa = any amino acid, and up  
to  
68 two amino acids can be missing  
70 <220> FEATURE:  
71 <221> NAME/KEY: MISC\_FEATURE  
72 <222> LOCATION: (10)..(14)  
73 <223> OTHER INFORMATION: Amino acid 15 is Z(-1) wherein Z(-1) = Arg, Lys, Gln, Asn,  
Thr,  
74 Met, Leu, Ile, Glu or Asp.  
76 <220> FEATURE:  
77 <221> NAME/KEY: misc\_feature  
78 <222> LOCATION: (15)..(15)  
79 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
81 <220> FEATURE:  
82 <221> NAME/KEY: MISC\_FEATURE  
83 <222> LOCATION: (16)..(16)  
84 <223> OTHER INFORMATION: Xaa can be any amino acid  
86 <220> FEATURE:  
87 <221> NAME/KEY: MISC\_FEATURE  
88 <222> LOCATION: (17)..(17)  
89 <223> OTHER INFORMATION: Amino acid 17 is Z2 wherein Z2 = Ser, Arg, Asn, Gln, Thr,  
Val,  
90 Ala, Asp or Glu.  
92 <220> FEATURE:  
93 <221> NAME/KEY: MISC\_FEATURE  
94 <222> LOCATION: (18)..(18)  
95 <223> OTHER INFORMATION: Amino acid 18 is Z3 wherein Z3 = His, Lys, Asn, Gln, Ser,  
Ala,  
96 Val, Thr, Asp, or Glu  
98 <220> FEATURE:  
99 <221> NAME/KEY: MISC\_FEATURE  
100 <222> LOCATION: (19)..(20)  
101 <223> OTHER INFORMATION: Xaa can be any amino acid  
103 <220> FEATURE:  
104 <221> NAME/KEY: MISC\_FEATURE  
105 <222> LOCATION: (21)..(21)  
106 <223> OTHER INFORMATION: Amino acid 21 is Z6 wherein Z6 = Arg, Lys, Gln, Asn, Thr,  
Tyr,  
107 Leu, Ile, Met, Glu or Asp.  
109 <220> FEATURE:  
110 <221> NAME/KEY: MISC\_FEATURE  
111 <222> LOCATION: (23)..(27)  
112 <223> OTHER INFORMATION: Amino acids 23-27 are Xaa wherein Xaa = any amino acid, and  
up to  
113 two amino acids can be missing.  
115 <220> FEATURE:  
116 <221> NAME/KEY: MISC\_FEATURE  
117 <222> LOCATION: (29)..(32)  
118 <223> OTHER INFORMATION: Xaa can be any amino acid  
120 <400> SEQUENCE: 2

W--> 122 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
123 1 5 10 15

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126 Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa  
 127                   20                                   25                                   30

130 <210> SEQ ID NO: 3  
 131 <211> LENGTH: 28  
 132 <212> TYPE: PRT  
 133 <213> ORGANISM: Artificial  
 135 <220> FEATURE:  
 136 <223> OTHER INFORMATION: Zinc finger domain  
 139 <220> FEATURE:  
 140 <221> NAME/KEY: MISC\_FEATURE  
 141 <222> LOCATION: (13)..(13)  
 142 <223> OTHER INFORMATION: Amino acid 13 is Z(-1) wherein Z(-1) = Arg, Lys, Gln, Asn,  
 Thr,  
 143           Met, Leu, Ile, Glu or Asp.  
 145 <220> FEATURE:  
 146 <221> NAME/KEY: MISC\_FEATURE  
 147 <222> LOCATION: (15)..(15)  
 148 <223> OTHER INFORMATION: Amino acid 15 is Z2 wherein Z2 = Ser, Arg, Asn, Gln, Thr,  
 Val,  
 149           Ala, Asp or Glu.  
 151 <220> FEATURE:  
 152 <221> NAME/KEY: MISC\_FEATURE  
 153 <222> LOCATION: (16)..(16)  
 154 <223> OTHER INFORMATION: Amino acid 16 is Z3 wherein Z3 = His, Lys, Asn, Gln, Ser,  
 Ala,  
 155           Val, Thr, Asp or Glu.  
 157 <220> FEATURE:  
 158 <221> NAME/KEY: MISC\_FEATURE  
 159 <222> LOCATION: (19)..(19)  
 160 <223> OTHER INFORMATION: Amino acid 19 is Z6 wherein Z6 = Arg, Lys, Gln, Asn, Thr,  
 Tyr,  
 161           Leu, Ile, Met, Glu or Asp.  
 163 <400> SEQUENCE: 3  
 W--> 165 Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa  
 166 1                   5                                   10                                   15  
 169 Leu Gln Xaa His Gln Arg Thr His Thr Gly Glu Lys  
 170                   20                                   25

173 <210> SEQ ID NO: 4  
 174 <211> LENGTH: 5  
 175 <212> TYPE: PRT  
 176 <213> ORGANISM: Artificial  
 178 <220> FEATURE:  
 179 <223> OTHER INFORMATION: peptide  
 181 <400> SEQUENCE: 4  
 183 Gly Gly Gly Gly Ser  
 184 1                   5  
 187 <210> SEQ ID NO: 5  
 188 <211> LENGTH: 11  
 189 <212> TYPE: PRT  
 190 <213> ORGANISM: Human immunodeficiency virus  
 193 <220> FEATURE:  
 194 <221> NAME/KEY: MISC\_FEATURE  
 195 <222> LOCATION: (1)..(11)

- see item #11 on  
 error  
 summary  
 sheet.

Invalid  
 Response

## RAW SEQUENCE LISTING

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Input Set : D:\1392-10-18-2.ST25.txt

Output Set: N:\CRF4\01262005\J500671.raw

```

196 <223> OTHER INFORMATION: HIV Tat protein domain
198 <400> SEQUENCE: 5
200 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
201 1          5          10
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 9
206 <212> TYPE: DNA
207 <213> ORGANISM: Human immunodeficiency virus
210 <220> FEATURE:
211 <221> NAME/KEY: misc_feature
212 <222> LOCATION: (1)..(9)
213 <223> OTHER INFORMATION: HIV DNA Binding Domain
215 <400> SEQUENCE: 6
216 gcagaagcc
219 <210> SEQ ID NO: 7
220 <211> LENGTH: 19
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial
224 <220> FEATURE:
225 <223> OTHER INFORMATION: DNA target sequence
227 <400> SEQUENCE: 7
228 gtgtgggtga gtgagtgtg
231 <210> SEQ ID NO: 8
232 <211> LENGTH: 19
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial
236 <220> FEATURE:
237 <223> OTHER INFORMATION: DNA target sequence
239 <400> SEQUENCE: 8
240 ggggctgggg gcggtgtct
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 7
245 <212> TYPE: PRT
246 <213> ORGANISM: Simian virus 40
249 <220> FEATURE:
250 <221> NAME/KEY: MISC_FEATURE
251 <222> LOCATION: (1)..(7)
252 <223> OTHER INFORMATION: Peptide from SV40 large T antigen
254 <400> SEQUENCE: 9
256 Pro Lys Lys Lys Arg Lys Val
257 1          5
260 <210> SEQ ID NO: 10
261 <211> LENGTH: 16
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Peptide, residues 43-58 of the Antennapeida homeodomain
protein
269 <220> FEATURE:
270 <221> NAME/KEY: MISC_FEATURE

```



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Input Set : D:\1392-10-18-2.ST25.txt

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271 <222> LOCATION: (1)..(16)  
 272 <223> OTHER INFORMATION: Peptide, residues 43-58 of the Antennapeida homeodomain protein

274 &lt;400&gt; SEQUENCE: 10

276 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys

277 1 5 10 15

280 &lt;210&gt; SEQ ID NO: 11

281 &lt;211&gt; LENGTH: 34

282 &lt;212&gt; TYPE: PRT

283 &lt;213&gt; ORGANISM: Herpes Simplex Virus

286 &lt;220&gt; FEATURE:

287 &lt;221&gt; NAME/KEY: MISC\_FEATURE

288 &lt;222&gt; LOCATION: (1)..(34)

289 &lt;223&gt; OTHER INFORMATION: Residues 267-300 of the HSV VP22 protein

291 &lt;400&gt; SEQUENCE: 11

293 Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr

294 1 5 10 15

297 Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro

298 20 25 30

301 Val Glu

305 &lt;210&gt; SEQ ID NO: 12

306 &lt;211&gt; LENGTH: 11

307 &lt;212&gt; TYPE: PRT

308 &lt;213&gt; ORGANISM: Artificial

310 &lt;220&gt; FEATURE:

311 &lt;223&gt; OTHER INFORMATION: Basic peptide with cellular uptake activity

314 &lt;220&gt; FEATURE:

315 &lt;221&gt; NAME/KEY: MISC\_FEATURE

316 &lt;222&gt; LOCATION: (1)..(11)

317 &lt;223&gt; OTHER INFORMATION: Basic peptide with cellular uptake activity

319 &lt;400&gt; SEQUENCE: 12

321 Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala

322 1 5 10

325 &lt;210&gt; SEQ ID NO: 13

326 &lt;211&gt; LENGTH: 9

327 &lt;212&gt; TYPE: PRT

328 &lt;213&gt; ORGANISM: Artificial

330 &lt;220&gt; FEATURE:

331 &lt;223&gt; OTHER INFORMATION: Basic peptide with cellular uptake activity, "R9"

333 &lt;400&gt; SEQUENCE: 13

335 Arg Arg Arg Arg Arg Arg Arg Arg Arg

336 1 5

339 &lt;210&gt; SEQ ID NO: 14

340 &lt;211&gt; LENGTH: 16

341 &lt;212&gt; TYPE: PRT

342 &lt;213&gt; ORGANISM: Artificial

344 &lt;220&gt; FEATURE:

345 &lt;223&gt; OTHER INFORMATION: D-penetratin peptide

348 &lt;220&gt; FEATURE:

349 &lt;221&gt; NAME/KEY: MISC\_FEATURE

↑  
 The type of errors shown exist throughout the sequence listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY  
 PATENT APPLICATION: US/10/500,671

DATE: 01/26/2005  
 TIME: 12:29:28

Input Set : D:\1392-10-18-2.ST25.txt  
 Output Set: N:\CRF4\01262005\J500671.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24,  
 Seq#:2; Xaa Pos. 1,2,3,5,6,7,8,10,11,12,13,14,15,16,17,18,19,20,21,23,24,25  
 Seq#:2; Xaa Pos. 26,27,29,30,31,32  
 Seq#:3; Xaa Pos. 13,15,16,19

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
 per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,7,8,10,12,13,14,15,16,17,18

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/500,671

DATE: 01/26/2005

TIME: 12:29:28

Input Set : D:\1392-10-18-2.ST25.txt

Output Set: N:\CRF4\01262005\J500671.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

M:341 Repeated in SeqNo=1

L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0

M:341 Repeated in SeqNo=2

L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0

M:341 Repeated in SeqNo=3